

## SEARCH REQUEST FORM

Scientific and Technical Information Center

Mailbox  
12E12

Requester's Full Name: Anne-Marie Baker Examiner #: 74977 Date: 4/18/01  
 Art Unit: 1632 Phone Number 306-9155 Serial Number: 08/963,288  
 Mail Box and Bldg/Room Location: 12D07 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

\*\*\*\*\*

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Expression Vector  
 Inventors (please provide full names): Norstedt et al

Earliest Priority Filing Date: 10/19/95

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

- Please perform an ~~eligo~~ search for  
 TTCTGAGAA

Limit to 12 mer or smaller.

POINT OF CONTACT:  
 BARB O'BRYEN  
 TECH. INFORMATION SPECIALIST  
 STIC CM1 12C14 308-4291

- Claim is directed to an enhancer element  
 consisting essentially of the nucleotide  
 sequence.

- There is no CRF for this and thus no SEQ ID NO.  
 for this 9-nucleotide sequence because the  
 sequence rules apply to sequences 10-nucleotides or  
 longer. Thus, this case is not required to comply  
 with the sequence rules. Or, looked at another way,  
 the case is in compliance because no CRF is required.

## STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>BOB</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>4-18-01</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>4-23-01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: <u>20</u>	Fulltext _____	Sequence Systems <u>IG, 14, 103</u>
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: <u>15</u>	Other _____	Other (specify) _____

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OY 1 ttctgaga 9  
Db 9 TTCTGAGA 1

## RESULT 2

US-08-369-796-34/c  
; Sequence 34, Application US/08369796  
; Patent No. 5716622  
; GENERAL INFORMATION:  
; APPLICANT: James E. Darnell, Jr.  
; APPLICANT: Zilong Wen  
; APPLICANT: Curt M. Horvath  
; APPLICANT: Zhong Zhong  
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauder & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/369,796  
; FILING DATE: 06-JAN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-116  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA synthetic probe  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-08-369-796-34

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
Db 9 TTCTGAGA 1

## RESULT 3

US-08-410-779B-35/c  
; Sequence 35, Application US/08410779B  
; Patent No. 5814517  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS  
; TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED  
; STREET: 9393 TOWNE CENTRE DRIVE  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 92121

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/410,779B  
; FILING DATE: 27-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/228,935  
; FILING DATE: 14-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JURGENSEN, THOMAS E  
; REGISTRATION NUMBER: 34,195  
; REFERENCE/DOCKET NUMBER: 016-0013A, US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 550-7675  
; TELEFAX: (619) 535-3906  
; INFORMATION FOR SEQ ID NO: 35:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
; DESCRIPTION: SYNTHETIC DNA"  
US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
Db 9 TTCTGAGA 1

## RESULT 4

US-08-852-091-34/c  
; Sequence 34, Application US/08852091  
; Patent No. 5883228  
; GENERAL INFORMATION:  
; APPLICANT: James E. Darnell, Jr.  
; APPLICANT: Zilong Wen  
; APPLICANT: Curt M. Horvath  
; APPLICANT: Zhong Zhong  
; TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
; TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauder & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/852,091  
; FILING DATE: 06-MAY-1997

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 21, 2001, 12:13:27 ; Search time 80.36 Seconds  
(without alignments)  
19.555 Million cell updates/sec

Title: SHORT  
Perfect score: 9  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 23618

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA:  
1: /cgn2\_6/ptodata/2/ina/5a.COMB.seq:\*  
2: /cgn2\_6/ptodata/2/ina/5b.COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6a.COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6b.COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	9	100.0	9	1 US-08-369-796-34	Sequence 34, Appl
C 3	9	100.0	9	1 US-08-410-779B-35	Sequence 35, Appl
C 4	9	100.0	9	2 US-08-852-091-34	Sequence 34, Appl
C 5	9	100.0	9	5 PCT-US95-04477-35	Sequence 35, Appl
C 6	9	100.0	9	5 PCT-US95-17025-34	Sequence 34, Appl
C 7	8	88.9	10	1 US-08-440-787A-85	Sequence 85, Appl
C 8	8	88.9	10	1 US-08-440-787A-86	Sequence 86, Appl
C 9	7.4	82.2	9	1 US-08-268-799-3	Sequence 3, Appl
C 10	7.4	82.2	9	1 US-08-411-020-12	Sequence 12, Appl
C 11	7.4	82.2	9	1 US-08-411-020-12	Sequence 12, Appl
C 12	7.4	82.2	9	1 US-08-411-020-13	Sequence 13, Appl
C 13	7.4	82.2	9	1 US-08-369-796-31	Sequence 31, Appl
C 14	7.4	82.2	9	1 US-08-369-796-34	Sequence 34, Appl
C 15	7.4	82.2	9	1 US-08-369-796-36	Sequence 36, Appl
C 16	7.4	82.2	9	1 US-08-369-796-38	Sequence 38, Appl
C 17	7.4	82.2	9	1 US-08-410-779B-31	Sequence 31, Appl
C 18	7.4	82.2	9	1 US-08-410-779B-35	Sequence 35, Appl
C 19	7.4	82.2	9	1 US-08-410-779B-51	Sequence 51, Appl
C 20	7.4	82.2	9	1 US-08-410-779B-51	Sequence 51, Appl
C 21	7.4	82.2	9	2 US-08-852-091-31	Sequence 31, Appl
C 22	7.4	82.2	9	2 US-08-852-091-34	Sequence 34, Appl
C 23	7.4	82.2	9	2 US-08-852-091-36	Sequence 36, Appl
C 24	7.4	82.2	9	2 US-08-852-091-38	Sequence 38, Appl
C 25	7.4	82.2	9	3 PCT-US95-04477-31	Sequence 31, Appl
C 26	7.4	82.2	9	5 PCT-US95-04477-35	Sequence 35, Appl
C 27	7.4	82.2	9	5 PCT-US95-04477-35	Sequence 35, Appl

28	7.4	82.2	9	5 PCT-US95-04477-51	Sequence 51, Appl
C 29	7.4	82.2	9	5 PCT-US95-04477-51	Sequence 51, Appl
C 30	7.4	82.2	9	5 PCT-US95-17025-31	Sequence 31, Appl
C 31	7.4	82.2	9	5 PCT-US95-17025-34	Sequence 34, Appl
C 32	7.4	82.2	9	5 PCT-US95-17025-36	Sequence 36, Appl
C 33	7.4	82.2	9	5 PCT-US95-17025-38	Sequence 38, Appl
C 34	7.4	82.2	10	1 US-08-410-779B-53	Sequence 53, Appl
C 35	7.4	82.2	10	1 US-08-410-779B-53	Sequence 53, Appl
C 36	7.4	82.2	10	5 PCT-US95-04477-53	Sequence 53, Appl
C 37	7.4	82.2	10	5 PCT-US95-04477-53	Sequence 53, Appl
C 38	7.4	82.2	11	1 US-08-394-191-9	Sequence 9, Appl
C 39	7.4	82.2	11	1 US-08-458-364-9	Sequence 9, Appl
C 40	7.4	82.2	11	3 US-09-177-431-17	Sequence 17, Appl
C 41	7.4	77.8	8	2 US-08-525-506-8	Sequence 8, Appl
C 42	7.4	77.8	8	3 US-08-859-954-516	Sequence 516, App
C 43	7.4	77.8	8	4 US-09-085-028-8	Sequence 8, Appl
C 44	7.4	77.8	10	1 US-08-222-177A-410	Sequence 410, App
C 45	7.4	77.8	11	2 US-08-232-016-4	Sequence 4, Appl

## ALIGNMENTS

RESULT 1  
US-08-411-020-13/C  
Sequence 13, Application US/08411020  
Patent No. 5712094  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
APPLICANT: CHAN, SHIN-SHAY TIAN  
TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
TITLE OF INVENTION: DETECTING MODULATORS OF CYTOKINE ACTION  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
City: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
US-08-411-020-13

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
| | | | |  
Db 9 TTCTGAGAA 1

## RESULT 2

US-08-369-796-34/C  
Sequence 34, Application US/08369796  
Patent No. 5716622  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ. ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-369-796-34

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
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Db 9 TTCTGAGAA 1

## RESULT 3

US-08-410-779B-35/C  
Sequence 35, Application US/08410779B  
Patent No. 5814517  
GENERAL INFORMATION:  
APPLICANT: SEIDEL, H. MARTI  
APPLICANT: LAMB, I. PETER  
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS  
TITLE OF INVENTION: RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 166  
CORRESPONDENCE ADDRESS:

ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED  
STREET: 9393 TOWNE CENTRE DRIVE  
CITY: SAN DIEGO  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92121

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/410,779B  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/228,935  
FILING DATE: 14-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: JURGENSEN, THOMAS E  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0013A.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ. ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
US-08-410-779B-35

Query Match 100.0%; Score 9; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
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Db 9 TTCTGAGAA 1

## RESULT 4

US-08-852-091-34/C  
Sequence 34, Application US/08852091  
Patent No. 5883228  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/852,091  
FILING DATE: 06-MAY-1997

CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/369,796  
FILING DATE: 06-JAN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-852-091-34

Query Match 100.0%; Score 9; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 5  
PCT-US95-04477-35/c  
Sequence 35, Application PC/TUS9504477  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS RESPONSIVE TO  
CYTOKINES AND METHODS FOR THEIR USE  
NUMBER OF SEQUENCES: 165  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04477  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/228,935  
FILING DATE: 14-APR-1994  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
PCT-US95-04477-35

Query Match 100.0%; Score 9; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 6  
PCT-US95-17025-34/c  
Sequence 34, Application PC/TUS9517025  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
APPLICANT: Zhong Zhong  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/17025  
FILING DATE: 28-DEC-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
PCT-US95-17025-34

Query Match 100.0%; Score 9; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.9e+07;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9  
|||||  
Db 9 TTCTGAGAA 1

RESULT 7  
US-08-440-787A-85/c  
Sequence 85, Application US/08440787A  
Patent No. 5770434  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Soluble Peptides Having Constrained,  
Secondary Conformation in Solution and Method of Making  
NUMBER OF SEQUENCES: 174  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,787A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,893  
FILING DATE: 10-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 1586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 85:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-787A-85

Query Match 88.9%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctgaga 9  
|||||||  
Db 10 TCTGAGA 3

RESULT 8  
US-08-440-787A-86  
Sequence 86, Application US/08440787A  
Patent No. 5770434  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Soluble Peptides Having Constrained,  
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making  
NUMBER OF SEQUENCES: 174  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/440,787A  
FILING DATE: 15-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/978,893  
FILING DATE: 10-NOV-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 1586  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-440-787A-86

Query Match 88.9%; Score 8; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.6e+03;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaga 8  
|||||||  
Db 3 TCTGAGA 10

RESULT 9  
US-08-268-799-3/c  
Sequence 3, Application US/08268799  
Patent No. 5654195  
GENERAL INFORMATION:  
APPLICANT: Sodroski, Joseph  
APPLICANT: Haseltine, William A.  
APPLICANT: Letvin, No. 5654195man  
TITLE OF INVENTION: Vectors Expressing Hybrid Viruses,  
TITLE OF INVENTION: Methods of Use And No. 5654195el Assays  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dike, Bronstejn, Roberts and Cushman  
STREET: 130 Water Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/268,799  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/887,505  
FILING DATE: 22-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I.  
REGISTRATION NUMBER: 30628  
REFERENCE/DOCKET NUMBER: 41858  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)523-3400  
TELEFAX: (617) 523-6440  
TELEX: 200291 stre ur  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
US-08-268-799-3

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;



Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | | | |  
Db 9 TTCTGAAA 1

RESULT 10  
US-08-411-020-12  
; Sequence 12, Application US/08411020  
; Patent No. 5712094  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; APPLICANT: CHAN, SHIN-SHAY TIAN  
; TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
; DETECTING MODULATORS OF CYTOKINE ACTION  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ligand Pharmaceuticals Incorporated  
; STREET: 9393 Towne Centre Drive  
; CITY: San Diego  
; STATE: California  
; COUNTRY: US  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/411,020  
; FILING DATE: 27-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jurgensen, Thomas E.  
; REGISTRATION NUMBER: 34,195  
; REFERENCE/DOCKET NUMBER: 016-0030.US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 550-7675  
; TELEFAX: (619) 535-3906  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
; DESCRIPTION: SYNTHETIC DNA"  
US-08-411-020-12

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | | | |  
Db 1 TTCTAGAA 9

RESULT 11  
US-08-411-020-12/C  
; Sequence 12, Application US/08411020  
; Patent No. 5712094  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; APPLICANT: CHAN, SHIN-SHAY TIAN  
; TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
; DETECTING MODULATORS OF CYTOKINE ACTION  
; NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Ligand Pharmaceuticals Incorporated  
STREET: 9393 Towne Centre Drive  
CITY: San Diego  
STATE: California  
COUNTRY: US  
ZIP: 92121  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/411,020  
FILING DATE: 27-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jurgensen, Thomas E.  
REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
DESCRIPTION: SYNTHETIC DNA"  
US-08-411-020-12

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | | | |  
Db 9 TTCTAGAA 1

RESULT 12  
US-08-411-020-13  
; Sequence 13, Application US/08411020  
; Patent No. 5712094  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; APPLICANT: CHAN, SHIN-SHAY TIAN  
; TITLE OF INVENTION: METHODS AND ASSOCIATED REAGENTS FOR  
; DETECTING MODULATORS OF CYTOKINE ACTION  
; NUMBER OF SEQUENCES: 59  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ligand Pharmaceuticals Incorporated  
; STREET: 9393 Towne Centre Drive  
; CITY: San Diego  
; STATE: California  
; COUNTRY: US  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/411,020  
; FILING DATE: 27-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jurgensen, Thomas E.

REGISTRATION NUMBER: 34,195  
REFERENCE/DOCKET NUMBER: 016-0030.US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
US-08-411-020-13

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgaga 9  
|||||  
DB 1 TTCTCAGAA 9

## RESULT 13

US-08-369-796-31/C  
Sequence 31, Application US/08369796  
Patent No. 5716622  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
APPLICANT: Zhong Zhong  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-369-796-31

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgaga 9  
|||||  
DB 9 TTCTGGGAA 1

## RESULT 14

US-08-369-796-34  
Sequence 34, Application US/08369796  
Patent No. 5716622  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.  
APPLICANT: Zilong Wen  
APPLICANT: Curt M. Horvath  
APPLICANT: Zhong Zhong  
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/369,796  
FILING DATE: 06-JAN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-116  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA synthetic probe  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-369-796-34

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
Best Local Similarity 88.9%; Pred. No. 1.9e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgaga 9  
|||||  
DB 1 TTCTCAGAA 9

RESULT 15  
US-08-369-796-36/C  
Sequence 36, Application US/08369796  
Patent No. 5716622  
GENERAL INFORMATION:  
APPLICANT: James E. Darnell, Jr.

APPLICANT: Zilong Wen  
 APPLICANT: Curt M. Horvath  
 APPLICANT: Zhong Zhong  
 TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL  
 NUMBER OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS  
 NUMBER OF SEQUENCES: 39  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/369,796  
 FILING DATE: 06-JAN-1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-116  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800  
 TELEFAX: 201 343-1684  
 TELEX: 133521  
 INFORMATION FOR SEQ ID NO: 36:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 9 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA synthetic probe  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-369-796-36

Query Match 82.2%; Score 7.4; DB 1; Length 9;  
 Best local Similarity 88.9%; Pred. No. 1.9e+07;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgaga 9  
 ||| |||||  
 DB 9 TTCGAGAA 1

Search completed: April 21, 2001, 13:12:32  
 Job time: 3545 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2001, 12:14:34 ; Search time 110.76 Seconds  
(without alignments)  
47.436 Million cell updates/sec

Title: SHORT  
Perfect score: 9  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 65774

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /SIDS2/gcgdata/geneseq/geneseq/NA1981.DAT:\*
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- 4: /SIDS2/gcgdata/geneseq/geneseq/NA1983.DAT:\*
- 5: /SIDS2/gcgdata/geneseq/geneseq/NA1984.DAT:\*
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- 7: /SIDS2/gcgdata/geneseq/geneseq/NA1986.DAT:\*
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- 18: /SIDS2/gcgdata/geneseq/geneseq/NA1997.DAT:\*
- 19: /SIDS2/gcgdata/geneseq/geneseq/NA1998.DAT:\*
- 20: /SIDS2/gcgdata/geneseq/geneseq/NA1999.DAT:\*
- 21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT:\*
- 22: /SIDS2/gcgdata/geneseq/geneseq/NA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	9	100.0	9	16 T14149	Cytokine responsiv
C 2	9	100.0	9	17 T41583	Cytokine activated
C 3	9	100.0	9	19 V56876	Regulatory element
C 4	8	88.9	11	20 V57642	NIL active EGS 6.
C 5	7.4	82.2	9	14 Q53424	SiVmac/HIV-1 junct
C 6	7.4	82.2	9	16 T14165	Cytokine responsiv
C 7	7.4	82.2	9	16 T14165	Cytokine responsiv
C 8	7.4	82.2	9	16 T14149	Cytokine responsiv
C 9	7.4	82.2	9	16 T14145	Cytokine responsiv
C 10	7.4	82.2	9	17 T41582	Cytokine activated
C 11	7.4	82.2	9	17 T41582	Cytokine activated

12	7.4	82.2	9	17 T41583	Cytokine activated
13	7.4	82.2	9	19 V56892	Regulatory element
C 14	7.4	82.2	9	19 V56892	Regulatory element
C 15	7.4	82.2	9	19 V56876	Regulatory element
C 16	7.4	82.2	9	19 V56872	Regulatory element
C 17	7.4	82.2	9	19 V11639	Regulatory element
C 18	7.4	82.2	9	21 C83341	Regulatory element
C 19	7.4	82.2	10	16 T14167	Cytokine responsiv
C 20	7.4	82.2	10	16 T14167	Cytokine responsiv
C 21	7.4	82.2	10	19 V56894	Regulatory element
C 22	7.4	82.2	10	19 V56894	Regulatory element
C 23	7.4	82.2	10	21 Z81339	Regulatory element
C 24	7.4	82.2	10	21 Z84449	Regulatory element
C 25	7.4	82.2	10	21 Z85845	Regulatory element
C 26	7.4	82.2	10	21 Z86651	Regulatory element
C 27	7.4	82.2	10	22 F36105	Regulatory element
C 28	7.4	82.2	10	22 F36115	Regulatory element
C 29	7.4	82.2	10	22 F40413	Regulatory element
C 30	7.4	82.2	10	22 F43208	Regulatory element
C 31	7.4	82.2	10	22 F43604	Regulatory element
C 32	7.4	82.2	10	22 F44027	Regulatory element
C 33	7.4	82.2	11	20 Z19018	Regulatory element
C 34	7.4	82.2	11	20 Z18836	Regulatory element
C 35	7.4	82.2	11	20 Z18737	Regulatory element
C 36	7.4	82.2	11	20 X25606	Regulatory element
C 37	7.4	82.2	11	21 A39462	Regulatory element
C 38	7.4	82.2	8	21 A81203	Regulatory element
C 39	7.4	82.2	9	21 A28766	Regulatory element
C 40	7.4	82.2	10	15 Q45107	Regulatory element
C 41	7.4	82.2	10	18 T66061	Regulatory element
C 42	7.4	82.2	10	20 X15564	Regulatory element
C 43	7.4	82.2	10	20 X02705	Regulatory element
C 44	7.4	82.2	10	21 C64164	Regulatory element
C 45	7.4	82.2	10	21 A56432	Regulatory element

## ALIGNMENTS

RESULT 1	T14149/C	T14149 standard; DNA; 9 BP.
XX	XX	XX
AC	T14149;	
XX	XX	XX
DT	29-MAR-1996 (first entry)	
XX	XX	XX
DE	Cytokine responsive DNA spacer regulatory element.	
XX	XX	XX
KW	Regulatory element; transcriptional regulatory protein;	
KW	signalling molecule; DNA spacer; agonist; antagonist; anaemia;	
KW	gene transcription; inflammation; cytopenia; cancer; ss.	
XX	XX	XX
OS	Synthetic.	
XX	XX	XX
PN	W09528482-A2.	
XX	XX	XX
PD	26-OCT-1995.	
XX	XX	XX
PF	10-APR-1995; 95WO-US04477.	
XX	XX	XX
PR	27-MAR-1995; 95US-0410780.	
PR	14-APR-1994; 94US-0228935.	
PA	(LIGA-) LIGAND PHARM INC.	
XX	XX	XX
PI	Lamb IP, Seidel HM;	
XX	XX	XX
DR	WPL; 1995-373797/48.	
XX	XX	XX
PT	DNA spacer regulatory elements responsive to cytokine(s) - for	
PT	detecting the presence of transcriptional regulatory protein in a	
PT	sample	

XX Claim 7: Page 125; 135bp; English.

PS

CC The present oligonucleotide comprises a regulatory element

CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an

CC activated transcriptional regulatory protein in response to a

CC signalling mol., i.e. a cytokine. This cytokine responsive DNA

CC spacer regulatory element can be used to detect the presence of

CC a transcriptional regulatory protein in a sample, and in assays

CC for (ant)agonists of gene transcription. The identified cpds.

CC may be used to treat cytokine-induced disease states, or to

CC ameliorate disease states caused by cytokine deficiency, e.g.

CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.

XX

SO Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 16; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.5e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9

DB 9 TTCTGAGAA 1

RESULT 2

T41583/c

ID T41583 standard; DNA; 9 BP.

XX

AC T41583;

XX

DT 04-JUN-1997 (first entry)

DE Cytokine activated STAT protein dependent DNA regulatory element.

XX

KM Regulatory element; protein; cytokine; responsive; host cell;

KM transfection; agonist; antagonist; mediated; transcription;

KM modulation; STAT; STAT5; STAT6; signalling pathway; ss.

XX

OS Synthetic.

XX

PN WO9630515-A1.

XX

PD 03-OCT-1996.

XX

PF 25-MAR-1996; 96WO-US04012.

XX

PT 27-MAR-1995; 95US-0411020.

XX

PA (LIGA-) LIGAND PHARM INC.

XX

PI Lamb IP, Seidel HM, Tian Chan S;

XX

DR WPI; 1996-455362/45.

XX

PT DNA construct for screening modulators of cytokine-mediated

PT transcription - contg. regulatory element and a cytokine-sensitive

XX

PS promoter operably linked to a heterologous gene

XX

Clalm 5; Page 61; 72pp; English.

CC A novel DNA construct comprises an oligonucleotide (ON) comprising

CC a regulatory element having the present sequence, operably linked

CC to a promoter, which is operably linked to a heterologous gene

CC (preferably a marker gene). The gene is under the transcriptional

CC control of the promoter and the ON sequence when the ON is bound by

CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,

CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,

CC IL-13 or IL-15. Cytokine responsive host cells transfected with the

CC DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene

CC transcription. In particular, they can be used to screen for

CC cytokine modulators involved in the STAT5 and/or STAT6 protein

CC signalling pathway.

XX

SO Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 17; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.5e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ttctgaga 9

DB 9 TTCTGAGAA 1

RESULT 3

V56876/c

ID V56876 standard; DNA; 9 BP.

XX

AC V56876;

XX

DT 02-DEC-1998 (first entry)

DE Regulatory element containing oligonucleotide #35.

XX

KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;

KM transcriptional control; STAT protein; screening; agonist; ss.

XX

OS Synthetic.

XX

PN US5814517-A.

XX

PD 29-SEP-1998.

XX

PF 27-MAR-1995; 95US-0410779.

XX

PT 27-MAR-1995; 95US-0410779.

XX

PR 14-APR-1994; 94US-0228935.

XX

PA (LIGA-) LIGAND PHARM INC.

XX

PI Lamb IP, Seidel HM;

XX

DR WPI; 1998-541763/46.

XX

PT DNA constructs containing cytokine-responsive regulatory elements -

PT useful in assays for transcription-regulating proteins or gene

XX

PS transcription agonists or antagonists

XX

Disclosure; Column 11; 58pp; English.

XX

CC V56842-V56976 and V61601-V61631 are oligonucleotides used in the

CC production of constructs comprising a cytokine-responsive regulatory

CC element linked to a promoter which is linked to a heterologous coding

CC sequence so that the coding sequence is under the transcriptional control

CC of the regulatory element and the promoter, where the regulatory element

CC has a nucleotide sequence selected from TTCNNGAA, TTAATTA, and TTCATTA

CC where N is A, T, C or G, and y = 3 or 4. The constructs can be used to

CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,

CC in a sample by contacting the sample with the construct so that the

CC protein binds to the regulatory element, and detecting or separating the

CC resulting complex. The cells can be used in screening assays for agonists

CC of gene transcription, in which the level of expression of the coding

CC sequence is measured in the presence and absence of a test compound or

CC in the presence of the corresponding cytokine.

XX

SO Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 100.0%; Score 9; DB 19; Length 9;

Best Local Similarity 100.0%; Pred. No. 6.5e+07;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Mon Apr 23 10:04:19 2001

short.rng

Page 3

QY 1 ttctgagaa 9  
 |||||  
 Db 9 TTCTGAGAA 1

RESULT 4  
 X77642/C  
 ID X77642 standard; DNA; 11 BP.  
 XX  
 AC X77642;  
 XX  
 DT 09-AUG-1999 (first entry)  
 XX  
 DE N1 active EGS 6.  
 XX  
 KM External guide sequence; EGS: target mRNA; identification; diagnostic;  
 KM Inactivation; essential gene; therapy; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN MO9927135-A2.  
 PD 03-JUN-1999.  
 PF 20-NOV-1998; 98MO-US24854.  
 PR 30-MAR-1998; 98US-0079851.  
 PR 21-NOV-1997; 97US-0976220.  
 PA (INNO-) INNOVIR LAB INC.  
 PI Kindt TJ, Nilsen TW, Robertson HD;  
 DR WPI; 1999-357853/30.  
 XX  
 PT Identifying and inhibiting functional nucleic acid molecules in  
 PT cells  
 PS Example 3; Page 28; 58pp; English.  
 XX  
 CC This invention describes a novel method allowing essential or functional  
 CC genes to be rapidly identified and inactivated. The method is able to  
 CC firstly identify most of the essential genes in an organism (i.e. a  
 CC bacteria or a eukaryote) needed for survival, and secondly it provides  
 CC for reducing or inactivating their expression. The method is able to  
 CC identify functional oligonucleotide molecules able to be used as  
 CC diagnostic reagents and therapeutics. The method provides a means for  
 CC identifying essential genes whose sequence is known only as part of a  
 CC genome with unknown function, as well as a means for identifying  
 CC functional oligonucleotide molecules. The method involves the use of a  
 CC nucleic acid molecule comprising (a) a first reporter gene encoding a  
 CC fusion protein comprising a protein of interest (itself translated from  
 CC an RNA of interest) and a reporter protein, a second reporter gene  
 CC encoding a second reporter protein, and (c) a targeting gene encoding a  
 CC functional oligonucleotide molecule such as an external guide sequence  
 CC (EGS), a ribozyme or an antisense RNA and targeted to the RNA of interest  
 CC at a site on the first reporter gene able to encode the RNA of interest.  
 CC  
 SQ Sequence 11 BP; 4 A; 4 C; 1 G; 2 T; 0 other;

Query Match 88.9%; Score 8; DB 20; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+04;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ttctgaga 8  
 |||||  
 Db 9 TTCTGAGA 2

RESULT 5  
 O53424/C  
 ID O53424 standard; DNA; 9 BP.

XX  
 AC O53424;  
 XX

DT 16-JUN-1994 (first entry)  
 XX

DE SIVmac/HIV-1 junction region #3.  
 XX

KM Junction fragment; vector; simian immunodeficiency virus; SIV; gag;  
 KM pol; vif; vpx; long terminal repeat; LTR; HIV-1; env; tat; rev;  
 KM nef; vpr; chimeric virus; replication competent; monkey; mandril;  
 KM macaque; disease progression; vaccine; epitope; immune response;  
 KM envelope glycoprotein; cytotoxic T lymphocyte; ss.  
 XX

OS Synthetic.  
 OS

PN MO9324632-A.  
 XX

PD 09-DEC-1993.  
 XX

PF 20-MAY-1993; 93MO-US04814.  
 XX

PR 22-MAY-1992; 92US-0887505.  
 XX

PA (DAND ) DANA FARBER CANCER INST INC.  
 PA (HARD ) HARVARD COLLEGE.  
 XX

PI Haseltine WA, Letvin N, Li J, Sodroski J;  
 XX

DR WPI; 1993-405823/50.  
 XX

PT Hybrid SIV-HIV-1 viral vectors - used to provide animal models  
 PT for HIV-1 infection or a therapeutic agents or in vaccines for  
 PT HIV-1  
 XX

PS Disclosure; Fig 1C; 72pp; English.  
 PS

CC The sequences given in O53422-28 represent junction fragments which  
 CC were used in the construction the vectors of the invention. These  
 CC vectors contain a 5' DNA segment which contains a sufficient number  
 CC of nucleotides corresponding to a simian immunodeficiency virus (SIV)  
 CC genome to encode a functional gag, pol, vif and vpx protein and has  
 CC a SIV long terminal repeat (LTR), and a 3' DNA segment which contains  
 CC a sufficient number of nucleotides corresponding to at least one  
 CC HIV-1 genome to encode a functional HIV-1 env, tat and rev protein  
 CC and a sufficient number of nucleotides corresponding to a SIV genome  
 CC to encode a functional nef protein and has a SIV LTR. The vector  
 CC further comprises a sufficient number of nucleotides corresponding to  
 CC the SIV genome to encode a functional SIV vpr protein. Vectors such  
 CC as these produce chimeric viruses containing HIV-1 components. As a  
 CC result of transfecting cells with these vectors, replication competent  
 CC viruses that are infectious in animal systems such as monkeys, eg.  
 CC mandrills, macaques, etc. can be produced. The vectors can be used for  
 CC creating an animal model for studying disease progression by HIV-1,  
 CC for screening for compounds exhibiting anti-HIV activity, for screening  
 CC for a vaccine against HIV infection and for determining the specific  
 CC epitopes of a HIV-1 envelope glycoprotein recognised by cytotoxic T  
 CC lymphocytes. They can also be used to boost immune response in a HIV  
 CC infected individual or as a vaccine to prevent infection.  
 CC  
 SQ Sequence 9 BP; 3 A; 1 C; 1 G; 4 T; 0 other;

Query Match 82.2%; Score 7.4; DB 14; Length 9;  
 Best Local Similarity 88.9%; Pred. No. 6.5e+07;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgagaa 9  
 |||||  
 Db 9 TTCTGAGAA 1

RESULT 6  
 T14165

```

ID T14165 standard; DNA; 9 BP.
XX
AC T14165;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KM Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KM gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN MO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for
PT detecting the presence of transcriptional regulatory protein in a
PT sample
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (ant)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match      82.2%; Score 7.4; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.5e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||
Db 1 ttctaagaa 9

RESULT 7
T14165/c
ID T14165 standard; DNA; 9 BP.
XX
AC T14165;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KM Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KM gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
PI

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```

XX
PN MO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;
XX
DR WPI; 1995-373797/48.
XX
PT DNA spacer regulatory elements responsive to cytokine(s) - for
PT detecting the presence of transcriptional regulatory protein in a
PT sample
XX
PS Claim 7; Page 125; 135pp; English.
XX
CC The present oligonucleotide comprises a regulatory element
CC TT(Nx)AA, where x is 4-7, and the regulatory element binds an
CC activated transcriptional regulatory protein in response to a
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA
CC spacer regulatory element can be used to detect the presence of
CC a transcriptional regulatory protein in a sample, and in assays
CC for (ant)agonists of gene transcription. The identified cpds.
CC may be used to treat cytokine-induced disease states, or to
CC ameliorate disease states caused by cytokine deficiency, e.g.
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.
XX
SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match      82.2%; Score 7.4; DB 16; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.5e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||
Db 9 TTTCTTAGAA 1

RESULT 8
T14149
ID T14149 standard; DNA; 9 BP.
XX
AC T14149;
XX
DT 29-MAY-1996 (first entry)
XX
DE Cytokine responsive DNA spacer regulatory element.
XX
KM Regulatory element; transcriptional regulatory protein;
KW signalling molecule; DNA spacer; agonist; antagonist; anaemia;
KM gene transcription; inflammation; cytopenia; cancer; ss.
XX
OS Synthetic.
XX
PN MO9528482-A2.
XX
PD 26-OCT-1995.
XX
PF 10-APR-1995; 95WO-US04477.
XX
PR 27-MAR-1995; 95US-0410780.
PR 14-APR-1994; 94US-0228935.
XX
PA (LIGA-) LIGAND PHARM INC.
XX
PI Lamb IP, Seidel HM;

```



XX DR WPI; 1995-373797/48.  
XX XX  
PT DNA spacer regulatory elements responsive to cytokine(s) - for  
PT detecting the presence of transcriptional regulatory protein in a  
PT sample  
XX PS Claim 7; Page 125; 135pp; English.  
XX XX  
CC The present oligonucleotide comprises a regulatory element  
CC TT(Nx)Aa, where x is 4-7, and the regulatory element binds an  
CC activated transcriptional regulatory protein in response to a  
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA  
CC spacer regulatory element can be used to detect the presence of  
CC a transcriptional regulatory protein in a sample, and in assays  
CC for (ant)agonists of gene transcription. The identified cpds.  
CC may be used to treat cytokine-induced disease states, or to  
CC ameliorate disease states caused by cytokine deficiency, e.g.  
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
XX XX  
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;  
  
Query Match                      82.2%; Score 7.4; DB 16; Length 9;  
Best Local Similarity    88.9%; Pred. No. 6.5e+07;  
Matches    8; Conservative    0; Mismatches    1; Indels    0; Gaps    0;  
  
QY    1    ttctgagaa 9  
      |||||  
      1 ttctcagaa 9  
Db  
  
RESULT    9  
T14145/C  
ID    T14145 standard; DNA; 9 BP.  
XX  
AC    T14145;  
XX  
DT    29-MAY-1996 (first entry)  
XX  
DE    Cytokine responsive DNA spacer regulatory element.  
XX  
XX    Regulatory element; transcriptional regulatory protein;  
KM signalling molecule; DNA spacer; agonist; antagonist; anaemia;  
KM gene transcription; inflammation; cytopenia; cancer; ss.  
XX  
OS    Synthetic.  
XX  
PN    WO9528482-A2.  
XX  
PD    26-OCT-1995.  
XX  
PF    10-APR-1995; 95WO-US04477.  
XX  
PR    27-MAR-1995; 95US-0410780.  
PR    14-APR-1994; 94US-0228935.  
XX  
PA    (LIGA-) LIGAND PHARM INC.  
XX  
PI    Lamb IP, Seidel HM;  
XX  
DR    WPI; 1995-373797/48.  
XX  
PT DNA spacer regulatory elements responsive to cytokine(s) - for  
PT detecting the presence of transcriptional regulatory protein in a  
PT sample  
XX  
PS Claim 7; Page 125; 135pp; English.  
XX  
CC The present oligonucleotide comprises a regulatory element  
CC TT(Nx)Aa, where x is 4-7, and the regulatory element binds an  
CC activated transcriptional regulatory protein in response to a  
CC signalling mol., i.e. a cytokine. This cytokine responsive DNA

CC spacer regulatory element can be used to detect the presence of  
CC a transcriptional regulatory protein in a sample, and in assays  
CC for (ant)agonists of gene transcription. The identified cpds.  
CC may be used to treat cytokine-induced disease states, or to  
CC ameliorate disease states caused by cytokine deficiency, e.g.  
CC inflammation, anaemia, cytopenia and (pre)cancerous conditions.  
XX XX  
SQ Sequence 9 BP; 3 A; 3 C; 1 G; 2 T; 0 other;  
  
Query Match                      82.2%; Score 7.4; DB 16; Length 9;  
Best Local Similarity    88.9%; Pred. No. 6.5e+07;  
Matches    8; Conservative    0; Mismatches    1; Indels    0; Gaps    0;  
  
QY    1    ttctgagaa 9  
      |||||  
      9 TTCGCGGAA 1  
Db  
  
RESULT    10  
T41582  
ID    T41582 standard; DNA; 9 BP.  
XX  
AC    T41582;  
XX  
DT    04-JUN-1997 (first entry)  
XX  
DE    Cytokine activated STAT protein dependent DNA regulatory element.  
XX  
XX    Regulatory element; protein; cytokine; responsive; host cell;  
KM transfection; agonist; antagonist; mediated; transcription;  
KM modulation; STAT; STAT5; STAT6; signalling pathway; ss.  
XX  
OS    Synthetic.  
XX  
PN    WO9630515-A1.  
XX  
PD    03-OCT-1996.  
XX  
PF    25-MAR-1996; 96WO-US04012.  
XX  
PR    27-MAR-1995; 95US-0411020.  
XX  
PA    (LIGA-) LIGAND PHARM INC.  
XX  
PI    Lamb IP, Seidel HM, Tian Chan S;  
XX  
DR    WPI; 1996-455362/45.  
XX  
PT DNA construct for screening modulators of cytokine-mediated  
PT transcription - contg. regulatory element and a cytokine-sensitive  
PT promoter operably linked to a heterologous gene  
XX  
PS Claim 5; Page 61; 72pp; English.  
XX  
CC A novel DNA construct comprises an oligonucleotide (ON) comprising  
CC a regulatory element having the present sequence, operably linked  
CC to a promoter, which is operably linked to a heterologous gene  
CC (preferably a marker gene). The gene is under the transcriptional  
CC control of the promoter and the ON sequence when the ON is bound by  
CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,  
CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,  
CC IL-13 or IL-15. Cytokine responsive host cells transfected with the  
CC DNA construct can be used to measure the ability of a compound to  
CC act as an agonist or antagonist of cytokine mediated gene  
CC transcription. In particular, they can be used to screen for  
CC cytokine modulators involved in the STAT5 and/or STAT6 protein  
CC signalling pathway.  
XX  
SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;  
  
Query Match                      82.2%; Score 7.4; DB 17; Length 9;

Best Local Similarity 88.9%; Pred. No. 6.5e+07;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | |  
Db 1 ttctaagaa 9

RESULT 11  
T41582/C  
ID T41582 standard; DNA; 9 BP.

AC T41582;

DT 04-JUN-1997 (first entry)

XX Cytokine activated STAT protein dependent DNA regulatory element.

XX Regulatory element; protein; cytokine; responsive; host cell;

KW transfection; agonist; antagonist; mediated; transcription;

KM modulation; STAT; STAT5; STAT6; signalling pathway; ss.

XX Synthetic.

OS

PN WO9630515-A1.

PD 03-OCT-1996.

PF 25-MAR-1996; 96WO-US04012.

PR 27-MAR-1995; 95US-0411020.

PS (LIGA-) LIGAND PHARM INC.

PI Lamb IP, Seidel HM, Tian Chan S;

DR WPI; 1996-455362/45.

XX DNA construct for screening modulators of cytokine-mediated

PT transcription - contg. regulatory element and a cytokine-sensitive

PT promoter operably linked to a heterologous gene

XX Claim 5; Page 61; 72pp; English.

PS A novel DNA construct comprises an oligonucleotide (ON) comprising

CC a regulatory element having the present sequence, operably linked

CC to a promoter, which is operably linked to a heterologous gene

CC (preferably a marker gene). The gene is under the transcriptional

CC control of the promoter and the ON sequence when the ON is bound by

CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,

CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,

CC IL-13 or IL-15. Cytokine responsive host cells transfected with the

CC DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene

CC transcription. In particular, they can be used to screen for

CC cytokine modulators involved in the STAT5 and/or STAT6 protein

CC signalling pathway.

SO Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match 82.2%; Score 7.4; DB 17; Length 9;

Best Local Similarity 88.9%; Pred. No. 6.5e+07;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | |  
Db 9 TTCTTAGAA 1

RESULT 12

T41583  
ID T41583 standard; DNA; 9 BP.

XX T41583;

AC T41582;

DT 04-JUN-1997 (first entry)

XX Cytokine activated STAT protein dependent DNA regulatory element.

XX Regulatory element; protein; cytokine; responsive; host cell;

KW transfection; agonist; antagonist; mediated; transcription;

KM modulation; STAT; STAT5; STAT6; signalling pathway; ss.

XX Synthetic.

OS

PN WO9630515-A1.

PD 03-OCT-1996.

PF 25-MAR-1996; 96WO-US04012.

PR 27-MAR-1995; 95US-0411020.

PS (LIGA-) LIGAND PHARM INC.

PI Lamb IP, Seidel HM, Tian Chan S;

DR WPI; 1996-455362/45.

XX DNA construct for screening modulators of cytokine-mediated

PT transcription - contg. regulatory element and a cytokine-sensitive

PT promoter operably linked to a heterologous gene

XX Claim 5; Page 61; 72pp; English.

PS A novel DNA construct comprises an oligonucleotide (ON) comprising

CC a regulatory element having the present sequence, operably linked

CC to a promoter, which is operably linked to a heterologous gene

CC (preferably a marker gene). The gene is under the transcriptional

CC control of the promoter and the ON sequence when the ON is bound by

CC a STAT protein activated in response to IL-2, IL-3, G-CSF, GM-CSF,

CC erythropoietin, thrombopoietin, or preferably IL-4, IL-7, IL-9,

CC IL-13 or IL-15. Cytokine responsive host cells transfected with the

CC DNA construct can be used to measure the ability of a compound to

CC act as an agonist or antagonist of cytokine mediated gene

CC transcription. In particular, they can be used to screen for

CC cytokine modulators involved in the STAT5 and/or STAT6 protein

CC signalling pathway.

SO Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

Query Match 82.2%; Score 7.4; DB 17; Length 9;

Best Local Similarity 88.9%; Pred. No. 6.5e+07;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | |  
Db 1 ttctcagaa 9

RESULT 13

V56892  
ID V56892 standard; DNA; 9 BP.

AC V56892;

DT 02-DEC-1998 (first entry)

XX Regulatory element containing oligonucleotide #51.

DE Cytokine-responsive regulatory; primer; promoter; detection; isolation;

KW transcriptional control; STAT protein; screening; agonist; ss.

XX Synthetic.

```

XX XX US5814517-A.
XX PN
XX XX
XX PD 29-SEP-1998.
XX PF 27-MAR-1995; 95US-0410779.
XX XX
XX PR 27-MAR-1995; 95US-0410779.
XX PR 14-APR-1994; 94US-0228935.
XX PA
XX (LIGA-) LIGAND PHARM INC.
XX PI
XX Lamb IP, Seidel HM;
XX DR WPI; 1998-541763/46.
XX PT
XX PT DNA constructs containing cytokine-responsive regulatory elements -
XX PT transcription agonists or antagonists
XX PS
XX PS Disclosure; Column 12; 58pp; English.
XX CC
XX CC V56842-V56976 and V61601-V61631 are oligonucleotides used in the
XX CC production of constructs comprising a cytokine-responsive regulatory
XX CC element linked to a promoter which is linked to a heterologous coding
XX CC sequence so that the coding sequence is under the transcriptional control
XX CC of the regulatory element and the promoter, where the regulatory element
XX CC has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA
XX CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to
XX CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
XX CC in a sample by contacting the sample with the construct so that the
XX CC protein binds to the regulatory element, and detecting or separating the
XX CC resulting complex. The cells can be used in screening assays for agonists
XX CC of gene transcription, in which the level of expression of the coding
XX CC sequence is measured in the presence and absence of a test compound or
XX CC in the presence of the corresponding cytokine.
XX SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match      82.2%; Score 7.4; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.5e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||
Db 1 ttctaagaa 9

RESULT 14
V56892/c
ID V56892 standard; DNA; 9 BP.
XX
XX V56892;
XX AC
XX XX
XX DT 02-DEC-1998 (first entry)
XX DE
XX DE Regulatory element containing oligonucleotide #51.
XX XX
XX KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;
XX KM transcriptional control; STAT protein; screening; agonist; ss.
XX OS
XX OS Synthetic.
XX XX
XX PN US5814517-A.
XX PD 29-SEP-1998.
XX PF 27-MAR-1995; 95US-0410779.
XX XX
XX PR 27-MAR-1995; 95US-0410779.
XX PR 14-APR-1994; 94US-0228935.
XX

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PA (LIGA-) LIGAND PHARM INC.
XX
XX PI
XX Lamb IP, Seidel HM;
XX DR WPI; 1998-541763/46.
XX PF
XX PT DNA constructs containing cytokine-responsive regulatory elements -
XX PT transcription agonists or antagonists
XX PS
XX PS Disclosure; Column 12; 58pp; English.
XX CC
XX CC V56842-V56976 and V61601-V61631 are oligonucleotides used in the
XX CC production of constructs comprising a cytokine-responsive regulatory
XX CC element linked to a promoter which is linked to a heterologous coding
XX CC sequence so that the coding sequence is under the transcriptional control
XX CC of the regulatory element and the promoter, where the regulatory element
XX CC has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA
XX CC where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to
XX CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,
XX CC in a sample by contacting the sample with the construct so that the
XX CC protein binds to the regulatory element, and detecting or separating the
XX CC resulting complex. The cells can be used in screening assays for agonists
XX CC of gene transcription, in which the level of expression of the coding
XX CC sequence is measured in the presence and absence of a test compound or
XX CC in the presence of the corresponding cytokine.
XX SQ Sequence 9 BP; 4 A; 1 C; 1 G; 3 T; 0 other;

Query Match      82.2%; Score 7.4; DB 19; Length 9;
Best Local Similarity 88.9%; Pred. No. 6.5e+07;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgagaa 9
   |||||
Db 9 TTCTTAGAA 1

RESULT 15
V56876
ID V56876 standard; DNA; 9 BP.
XX
XX V56876;
XX AC
XX XX
XX DT 02-DEC-1998 (first entry)
XX DE
XX DE Regulatory element containing oligonucleotide #35.
XX KM
XX KM Cytokine-responsive regulatory; primer; promoter; detection; isolation;
XX KM transcriptional control; STAT protein; screening; agonist; ss.
XX OS
XX OS Synthetic.
XX PN US5814517-A.
XX PD 29-SEP-1998.
XX PF 27-MAR-1995; 95US-0410779.
XX XX
XX PR 27-MAR-1995; 95US-0410779.
XX PR 14-APR-1994; 94US-0228935.
XX XX
XX PA (LIGA-) LIGAND PHARM INC.
XX PI
XX Lamb IP, Seidel HM;
XX DR WPI; 1998-541763/46.
XX PT
XX PT DNA constructs containing cytokine-responsive regulatory elements -
XX PT transcription agonists or antagonists

```

PS Disclosure: Column 11: 58pp; English.

XX  
CC V56842-V56976 and V61601-V61631 are oligonucleotides used in the  
CC production of constructs comprising a cytokine-responsive regulatory  
CC element linked to a promoter which is linked to a heterologous coding  
CC sequence so that the coding sequence is under the transcriptional control  
CC of the regulatory element and the promoter, where the regulatory element  
CC has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA  
CC where N is A, T, C or G, and Y - 3 or 4. The constructs can be used to  
CC detect or isolate transcription-regulating proteins, e.g. STAT proteins,  
CC in a sample by contacting the sample with the construct so that the  
CC protein binds to the regulatory element, and detecting or separating the  
CC resulting complex. The cells can be used in screening assays for agonists  
CC of gene transcription, in which the level of expression of the coding  
CC sequence is measured in the presence and absence of a test compound or  
CC in the presence of the corresponding cytokine.

XX  
SQ Sequence 9 BP; 3 A; 2 C; 1 G; 3 T; 0 other;

# Query Match

Best Local Similarity 82.2%; Score 7.4; DB 19; Length 9;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttctgagaa 9  
| | | | |  
Db 1 ttctcagaa 9

Search completed: April 21, 2001, 13:14:35  
Job time: 3601 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2001, 11:42:58 ; Search time 1240.49 Seconds  
(without alignments)  
44.677 Million cell updates/sec

Title: SHORT  
Perfect score: 9  
Sequence: 1 ttctgagaa 9

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 3078962356 residues

Total number of hits satisfying chosen parameters: 15938

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

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- 2: gb\_ba2:\*
- 3: gb\_ba3:\*
- 4: gb\_in1:\*
- 5: gb\_in2:\*
- 6: gb\_in3:\*
- 7: gb\_om:\*
- 8: gb\_ov:\*
- 9: gb\_pat1:\*
- 10: gb\_pat2:\*
- 11: gb\_ph:\*
- 12: gb\_pi1:\*
- 13: gb\_pi2:\*
- 14: gb\_pi3:\*
- 15: gb\_pi4:\*
- 16: em\_ba1:\*
- 17: em\_ba2:\*
- 18: em\_fun:\*
- 19: em\_higo\_hum:\*
- 20: em\_higo\_inv:\*
- 21: em\_higo\_rod:\*
- 22: em\_hig\_hum1:\*
- 23: em\_hig\_hum2:\*
- 24: em\_hig\_hum3:\*
- 25: em\_hig\_hum4:\*
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- 31: em\_hig\_inv2:\*
- 32: em\_hig\_other:\*
- 33: em\_hig\_rod:\*
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- 51: em\_un:\*
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- 53: gb\_sts1:\*
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- 58: gb\_v1:\*
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- 86: gb\_pi2:\*
- 87: gb\_pi3:\*
- 88: gb\_pi4:\*
- 89: gb\_pi5:\*
- 90: gb\_pi6:\*
- 91: gb\_pi7:\*
- 92: gb\_pi8:\*
- 93: gb\_pi9:\*
- 94: gb\_pi1:\*
- 95: gb\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
c 1	7.4	82.2	9	9	AX041991	AX041991 Sequence
c 2	7.4	82.2	10	9	AR043683	AR043683 Sequence
c 3	7.4	82.2	10	9	AR043683	AR043683 Sequence
c 4	7.4	82.2	11	9	AR097294	AR097294 Sequence
c 5	7.4	82.2	11	9	AX063653	AX063653 Sequence
c 6	7.4	82.2	11	9	AX063656	AX063656 Sequence
c 7	7.4	82.2	11	10	I39722	I39722 Sequence
c 8	7.4	82.2	11	10	I55839	I55839 Sequence
c 9	7.4	82.2	12	93	S75371	S75371 beta-hexosa
c 10	7.4	82.2	12	93	S75371	S75371 beta-hexosa
c 11	7.4	82.2	8	9	AR101594	AR101594 Sequence

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C 12 7 77.8 10 9 A41392 A41392 Sequence 18
C 13 7 77.8 11 9 A24764 A24764 Oligonucleo
C 14 7 77.8 11 9 AR074369 AR074369 Sequence
C 15 7 77.8 12 9 A06058 A06058 Synthetic p
C 16 7 77.8 12 9 A06059 A06059 Synthetic p
C 17 7 77.8 12 9 A16601 A16601 Nucleotide
C 18 7 77.8 12 9 A16602 A16602 Nucleotide
C 19 7 77.8 12 9 A16603 A16603 Nucleotide
C 20 7 77.8 12 9 A16604 A16604 Nucleotide
C 21 6.6 73.3 12 10 A01725 A01725 Vector DNA
C 22 6.6 73.3 12 9 A01735 A01735 Vector DNA
C 23 6.4 71.1 10 9 AR101591 AR101591 Sequence
C 24 6.4 71.1 10 10 E17310 E17310 PCR primer
C 25 6.4 71.1 11 9 A62062 A62062 Sequence 48
C 26 6.4 71.1 12 9 A71450 A71450 Sequence 9
C 27 6.4 71.1 12 9 A87963 A87963 Sequence 11
C 28 6.4 71.1 12 9 A89930 A89930 Sequence 11
C 29 6.4 71.1 12 9 AX059219 AX059219 Sequence
C 30 6.4 71.1 12 10 AX069323 AX069323 Sequence
C 31 6.4 71.1 12 10 I39779 I39779 Sequence 52
C 32 6.6 77.7 8 9 AR101242 AR101242 Sequence
C 33 6.6 77.7 8 9 AR101244 AR101244 Sequence
C 34 6.6 77.7 8 9 AR101294 AR101294 Sequence
C 35 6.6 77.7 8 9 AR101393 AR101393 Sequence
C 36 6.6 77.7 8 9 AR101394 AR101394 Sequence
C 37 6.6 77.7 8 9 AR101395 AR101395 Sequence
C 38 6.6 77.7 8 9 AR101540 AR101540 Sequence
C 39 6.6 77.7 8 9 AR101582 AR101582 Sequence
C 40 6.6 77.7 8 9 AR101590 AR101590 Sequence
C 41 6.6 77.7 9 93 S75375 S75375 beta-hexosa
C 42 6.6 77.7 10 9 AR042901 AR042901 Sequence
C 43 6.6 77.7 10 10 I22208 I22208 Sequence 22
C 44 6.6 77.7 10 10 I75076 I75076 Sequence 6
C 45 6.6 77.7 10 59 S77264 S77264 {3' terminu

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## ALIGNMENTS

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RESULT 1
LOCUS AX041991/c
DEFINITION Sequence 21 from Patent WO0065067.
ACCESSION AX041991
VERSION AX041991.1 GI:11340754
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 9)
JOURNAL Nelson, P.S., Hood, L. and Lin, B.
FEATURES
source Prostate-specific polynucleotides, polypeptides and their methods
of use Patent: WO 0065067-A 21 02-NOV-2000;
The University of Washington (US)
LOCATION/Qualifiers
protein_bind 1..9
BASE COUNT 3 a 3 c 1 g 2 t
ORIGIN

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Query Match 82.2%; Score 7.4; DB 9; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.6e+09;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ttctgagaa 9
DB 9 TTCTGGGAA 1

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RESULT 2
LOCUS AR043683
DEFINITION Sequence 53 from patent US 5814517.
ACCESSION AR043683
VERSION AR043683.1 GI:5964691
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Seidel, H. Martin and Lamb, I. Peter.
TITLE DNA spacer regulatory elements responsive to cytokines and methods
for their use
JOURNAL Patent: US 5814517-A 53 29-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 4 a 1 c 1 g 4 t
ORIGIN

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Query Match 82.2%; Score 7.4; DB 9; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ttctgagaa 9
DB 2 TTCTAGAGAA 10

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RESULT 3
LOCUS AR043683/c
DEFINITION Sequence 53 from patent US 5814517.
ACCESSION AR043683
VERSION AR043683.1 GI:5964691
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Seidel, H. Martin and Lamb, I. Peter.
TITLE DNA spacer regulatory elements responsive to cytokines and methods
for their use
JOURNAL Patent: US 5814517-A 53 29-SEP-1998;
FEATURES
source Location/Qualifiers
BASE COUNT 4 a 1 c 1 g 4 t
ORIGIN

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Query Match 82.2%; Score 7.4; DB 9; Length 10;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ttctgagaa 9
DB 10 TTCTAGAGAA 2

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RESULT 4
LOCUS AR097294
DEFINITION Sequence 17 from patent US 6071700.
ACCESSION AR097294
VERSION AR097294.1 GI:12806024
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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QY      1 ttctgagaa 9
      111111111
Db      2 TTCTGGGAA 10

RESULT  9
LOCUS   S75371      12 bp      mRNA      PRI      07-MAY-1993
DEFINITION beta-hexosaminidase A (exon 8) [human, mRNA Partial Mutant, 12 nt].
ACCESSION S75371
VERSION   S75371.1 GI:241964
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Akil,S., Chelly,J., Lacorte,J.M., Poenaru,L. and Kahn,A.
TITLE     Seven novel Tay-Sachs mutations detected by chemical mismatch
          cleavage of PCR-amplified cDNA fragments
JOURNAL   Genomics 11 (1), 124-134 (1991)
MEDLINE   92112203
REMARK    Genbank staff at the National Library of Medicine created this
          entry [NCBI glibseq 75371] from the original journal article.
          This sequence comes from Figure 4.D.
          Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /partial
            /gene="beta-hexosaminidase A"

BASE COUNT      5 a      2 c      1 g      4 t
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4
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10
11
12

Query Match      82.2%; Score 7.4; DB 93; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.1e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ttctgagaa 9
      111111111
Db      4 TTCTTAGAA 12

RESULT 10
LOCUS   S75371      12 bp      mRNA      PRI      07-MAY-1993
DEFINITION beta-hexosaminidase A (exon 8) [human, mRNA Partial Mutant, 12 nt].
ACCESSION S75371
VERSION   S75371.1 GI:241964
KEYWORDS
SOURCE   human.
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 12)
AUTHORS   Akil,S., Chelly,J., Lacorte,J.M., Poenaru,L. and Kahn,A.
TITLE     Seven novel Tay-Sachs mutations detected by chemical mismatch
          cleavage of PCR-amplified cDNA fragments
JOURNAL   Genomics 11 (1), 124-134 (1991)
MEDLINE   92112203
REMARK    Genbank staff at the National Library of Medicine created this
          entry [NCBI glibseq 75371] from the original journal article.
          This sequence comes from Figure 4.D.
          Location/Qualifiers
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            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /partial
            /gene="beta-hexosaminidase A"

BASE COUNT      3 a      3 c      2 g      2 t
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5
6
7
8
9
10
11
12

Query Match      77.8%; Score 7; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 ttctgaga 8
      111111111
Db      1 TCTGAGA 7

RESULT 12
LOCUS   A41392      10 bp      DNA      PAT      05-MAR-1997
DEFINITION Sequence 18 from Patent WO9426928.
ACCESSION A41392
VERSION   A41392.1 GI:2297111
KEYWORDS
SOURCE   synthetic construct.
          synthetic construct.
          artificial sequence.
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS   Strauss,M. and Bauer,D.
TITLE     COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
          DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
          Patent: WO 9426928-A 18 24-NOV-1994;
          MAX PLANCK GESELLSCHAFT (DE)
          Other publication DE 4317414 940421.
          Location/Qualifiers
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            /db_xref="taxon:32630"

BASE COUNT      3 a      3 c      2 g      2 t
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9
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11
12

Query Match      77.8%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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BASE COUNT      5 a      2 c      1 g      4 t
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8
9
10
11
12

Query Match      82.2%; Score 7.4; DB 93; Length 12;
Best Local Similarity 88.9%; Pred. No. 1.1e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 ttctgagaa 9
      111111111
Db      12 TTCTAGAA 4

RESULT 11
LOCUS   AR101594      8 bp      DNA      PAT      14-FEB-2001
DEFINITION Sequence 516 from patent US 6083695.
ACCESSION AR101594
VERSION   AR101594.1 GI:12812392
KEYWORDS
SOURCE   Unknown.
          Unknown.
ORGANISM
REFERENCE 1 (bases 1 to 8)
AUTHORS   Hardin,S.Houck, Homayouni,R. and Hardin,P.Eric.
TITLE     Optimized primer library for gene sequencing and method of using
          same
JOURNAL   Patent: US 6083695-A 516 04-JUL-2000;
          Location/Qualifiers
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            /partial
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BASE COUNT      2 a      2 c      2 g      2 t
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6
7
8
9
10
11
12

Query Match      77.8%; Score 7; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ttctgaga 8
      111111111
Db      1 TCTGAGA 7

RESULT 12
LOCUS   A41392      10 bp      DNA      PAT      05-MAR-1997
DEFINITION Sequence 18 from Patent WO9426928.
ACCESSION A41392
VERSION   A41392.1 GI:2297111
KEYWORDS
SOURCE   synthetic construct.
          synthetic construct.
          artificial sequence.
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS   Strauss,M. and Bauer,D.
TITLE     COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
          DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT
          Patent: WO 9426928-A 18 24-NOV-1994;
          MAX PLANCK GESELLSCHAFT (DE)
          Other publication DE 4317414 940421.
          Location/Qualifiers
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            /organism="synthetic construct"
            /db_xref="taxon:32630"

BASE COUNT      3 a      3 c      2 g      2 t
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4
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6
7
8
9
10
11
12

Query Match      77.8%; Score 7; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 2 tctgaga 8  
 Db 9 TCTGAGA 3

RESULT 13  
 LOCUS A24764 11 bp DNA PAT 24-FEB-1995  
 DEFINITION oligonucleotide PS39.  
 ACCESSION A24764  
 VERSION A24764.1 GI:833668  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS  
 TITLE MODIFIED GENES AND THEIR EXPRESSION IN PLANT CELLS  
 JOURNAL Patent: WO 9309218-A 4 13-MAY-1993;  
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 BASE COUNT 3 a 3 c 2 g 3 t  
 ORIGIN

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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 ctgagaa 9  
 Db 11 CTGAGAA 5

RESULT 14  
 LOCUS AR074369/c 11 bp DNA PAT 28-AUG-2000  
 DEFINITION Sequence 4 from patent US 5952547.  
 ACCESSION AR074369  
 VERSION AR074369.1 GI:10001124  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 11)  
 AUTHORS Cornillissen,M., Soetaert,P., Stam,M., Dockx,J. and Van Aarsen,R.  
 TITLE Modified Bacillus thuringiensis genes with improved expression in  
 plant cells, methods of production on and use  
 JOURNAL Patent: US 5952547-A 4 14-SEP-1999;  
 FEATURES Location/Qualifiers  
 source 1..11  
 /organism="unknown"  
 BASE COUNT 3 a 3 c 2 g 3 t  
 ORIGIN

Query Match 77.8%; Score 7; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 ctgagaa 9  
 Db 11 CTGAGAA 5

RESULT 15  
 LOCUS A06058 12 bp DNA PAT 25-MAY-1993  
 DEFINITION Synthetic primer 476-487.  
 ACCESSION A06058  
 VERSION A06058.1 GI:411190

KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM synthetic construct.  
 REFERENCE 1 (bases 1 to 12)  
 AUTHORS Hudson,P.J., Haley,J.D., Mall,H.D. and Shine,J.  
 TITLE Molecular cloning and characterization of the gene sequence coding  
 for porcine relaxin  
 JOURNAL Patent: EP 0086649-A 8 24-AUG-1983;  
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 BASE COUNT 2 a 2 c 5 g 3 t  
 ORIGIN

Query Match 77.8%; Score 7; DB 9; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+06;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 tctgaga 8  
 Db 3 TCTGAGA 9

Search completed: April 21, 2001, 13:07:39  
 Job time: 5081 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 21, 2001, 11:14:44 ; Search time 1100.03 Seconds  
(without alignments)  
1.196 Million cell updates/sec

Title: SHORT

Perfect score: 9

Sequence: 1 ttctgagaa 9

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 73081774 residues

Total number of hits satisfying chosen parameters: 308

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*  
12: gb\_est12:\*  
13: gb\_est13:\*  
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15: gb\_est15:\*  
16: gb\_est16:\*  
17: gb\_est17:\*  
18: gb\_est18:\*  
19: gb\_est19:\*  
20: gb\_est20:\*  
21: gb\_est21:\*  
22: gb\_est22:\*  
23: gb\_est23:\*  
24: gb\_est24:\*  
25: gb\_est25:\*  
26: gb\_est26:\*  
27: gb\_est27:\*  
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33: gb\_est33:\*  
34: gb\_est34:\*  
35: gb\_est35:\*  
36: gb\_est36:\*  
37: gb\_est37:\*  
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39: gb\_est39:\*  
40: gb\_est40:\*  
41: gb\_est41:\*  
42: gb\_est42:\*  
43: gb\_est43:\*

44: em\_esthum10:\*  
45: em\_esthum11:\*  
46: em\_esthum12:\*  
47: em\_esthum13:\*  
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54: em\_esthum20:\*  
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57: em\_esthum23:\*  
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188: gb-est119:*
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192: em-gss-pro:*
193: em-gss-rod1:*
194: em-gss-rod2:*
195: em-gss-rod3:*
196: em-gss-rod4:*
197: em-gss-rod5:*
198: em-gss-rod6:*
199: em-gss-rod7:*
200: em-gss-rod8:*
201: em-gss-rod9:*
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203: em-gss-rod11:*
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227: em-gss-rod35:*
228: em-gss-rod36:*
229: em-gss-rod37:*
230: em-gss-rod38:*
231: em-gss-rod39:*
232: em-gss-rod40:*
233: em-gss-rod41:*
234: em-gss-rod42:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5.4	60.0	12	113	AW250557	AW250557 2821633.5
2	4.8	53.3	11	60	HSM007328	A1042478 Homo sapi
3	4.8	53.3	11	60	HSM007344	A1042494 Homo sapi
4	4.8	53.3	11	60	HSM007376	A1042526 Homo sapi
5	4.4	48.9	11	60	HSM007328	A1042478 Homo sapi
6	4.4	48.9	11	60	HSM007344	A1042494 Homo sapi
7	4.4	48.9	11	60	HSM007376	A1042526 Homo sapi
8	4.4	48.9	11	113	AW250935	AW250935 2821359.3
9	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
10	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
11	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
12	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
13	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
14	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
15	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
16	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
17	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
18	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi
19	4.4	48.9	12	60	HSM007404	A1042554 Homo sapi

C 19	3.8	42.2	12	113	AM250557	2821633.5
C 20	3.8	42.2	12	175	C51419	C51419 Yuj1
C 21	3.4	37.8	7	60	HSM007412	AL042562 Homo sapi
C 22	3.4	37.8	10	60	HSM004456	AL039980 Homo sapi
C 23	3.4	37.8	10	60	HSM007587	AL042737 Homo sapi
C 24	3.4	37.8	10	112	AM248243	AM248243 2819618.5
C 25	3.4	37.8	11	60	HSM008167	AL043317 Homo sapi
C 26	3.4	37.8	11	112	AM245969	AM245969 2822722.3
C 27	3.4	37.8	11	112	AM247612	AM247612 2819980.5
C 28	3.4	37.8	11	112	AM247933	AM247933 2820656.3
C 29	3.4	37.8	11	112	AM249647	AM249647 2819740.3
C 30	3.4	37.8	11	112	AM249797	AM249797 2819795.3
C 31	3.4	37.8	11	113	AM250442	AM250442 2822410.3
C 32	3.4	37.8	12	60	HSM007351	AL042501 Homo sapi
C 33	3.4	37.8	12	60	HSM007351	AL042501 Homo sapi
C 34	3.4	37.8	12	60	HSM007936	AL043086 Homo sapi
C 35	3.4	37.8	12	60	HSM008119	AL043289 Homo sapi
C 36	3.4	37.8	12	106	AU061224	AU061224 AU061224
C 37	3.4	37.8	12	112	AM249871	AM249871 2821560.3
C 38	3.4	37.8	12	113	AM250760	AM250760 2822521.3
C 39	3.4	37.8	12	113	AM250791	AM250791 2822383.3
C 40	3.4	37.8	12	201	A0050979	A0050979 nBXD0004d
C 41	3.4	37.8	12	118	AM672605	AM672605 2XA Expla
C 42	3.3	33.3	4	60	HSM010467	AL045617 Homo sapi
C 43	3.3	33.3	4	118	AM672622	AM672622 73C Expla
C 44	3.3	33.3	5	60	HSM007310	AL042460 Homo sapi
C 45	3.3	33.3	5	60	HSM007310	AL042460 Homo sapi

## ALIGNMENTS

RESULT 1  
 LOCUS AM250557 12 bp mRNA EST 07-JAN-2000  
 DEFINITION 2821633.5prime NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:2821633 5',  
 mRNA sequence.  
 ACCESSION AM250557  
 VERSION AM250557.1 GI:6593550  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 12)  
 NIH-MGC http://mgc.nci.nih.gov/  
 TITLE Unpublished (1999)  
 JOURNAL Other ESTs: 2821633.3prime  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Tel: (301) 496-1550  
 Email: Robert.Strausberg@nih.gov

Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling  
 Honn/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.  
 Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing  
 Project Clone distribution: MGC clone distribution information can  
 be found through the I.M.A.G.E. Consortium/LNL at:  
 www.bio.ln1.gov/bdrp/image/image.html Base Calling / Quality  
 Scores: PHRED from University of Washington Genome Center. Vector  
 Trimming: cross\_match from University of Washington Genome Center  
 PHRAP suite. Poly-T identification: patmatch.pl from Berkeley  
 Drosophila Genome Project. University of Washington Genome Center:  
 http://www.genome.washington.edu Low Quality Sequence: 0 contiguous  
 PHRED high quality bases following vector sequence. Very low  
 Quality Sequence: trace file contained 12 contiguous distinct peaks  
 following vector sequence.  
 Plate: LICM7 row: F column: 2.

## FEATURES

source  
 1.12  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2821633"  
 /clone\_lib="NIH\_MGC\_7"

/tissue\_type="small cell carcinoma"  
 /cell\_line="MGC3"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: lung; Vector: pOTB; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(C). Size-selected >500bp for average  
 insert size 1.8kb. Library constructed by Ling Hong in  
 the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."  
 BASE COUNT 2 a 1 c 4 g 5 t

Query Match 60.0%; Score 5.4; DB 113; Length 12;  
 Best Local Similarity 85.7%; Pred. No. 1.6e+07;  
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ttctgag 7  
 || |||||  
 Db 5 ttttgag 11

RESULT 2  
 HSM007328/C  
 ID HSM007328 standard; RNA; EST; 11 BP.

AC AL042478;  
 XX AL042478.1  
 SV

DT 12-MAR-1999 (Rel. 59, Created)  
 DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)  
 XX  
 DE Homo sapiens mRNA; EST DKFZp434F1721\_r1 (from clone DKFZp434F1721)  
 XX  
 KW EST; expressed sequence tag.

OS Homo sapiens (human)  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;  
 OC Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 XX  
 RN [1]  
 RP 1-11  
 RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.,  
 Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY  
 CC Clone from S. Wiemann, sequenced by LMU within the cDNA  
 CC sequencing consortium of the German Genome Project  
 CC No sl sequence available  
 CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de

XX Key Location/Qualifiers  
 FH  
 FT source 1.11  
 FT /db\_xref="taxon:9606"  
 FT /organism="Homo sapiens"  
 FT /clone="DKFZp434F1721"  
 FT /clone\_lib="434 (synonym: hies3). Vector pSport1; host  
 FT DH10B; sites NotI + SalI"  
 FT /dev\_stage="adult"  
 FT /tissue\_type="testis"

XX Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 53.3%; Score 4.8; DB 60; Length 11;  
 Best Local Similarity 75.0%; Pred. No. 4.2e+07;

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Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ttctgaga 8
   ||| |||
Db 9 TTCCGAAA 2

RESULT 3
HSM007344/C
ID HSM007344 standard; RNA; EST; 11 BP.
AC AL042494;
XX
SV AL042494.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
RL 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434G1721_r1 (from clone DKFZp434G1721)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-11
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de
XX
XX Key Location/Qualifiers
FH 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434G1721"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
XX
SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 53.3%; Score 4.8; DB 60; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.2e+07;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ttctgaga 8
   ||| |||
Db 9 TTCCGAAA 2

RESULT 4
HSM007376/C
ID HSM007376 standard; RNA; EST; 11 BP.
AC AL042526;
XX
SV AL042526.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
RL 12-MAR-1999 (Rel. 59, Last updated, Version 1)

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```

XX Homo sapiens mRNA; EST DKFZp434H0321_r1 (from clone DKFZp434H0321)
DE
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OS
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-11
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No sl sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de
XX
XX Key Location/Qualifiers
FH 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434H0321"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /issue_type="testis"
XX
SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 53.3%; Score 4.8; DB 60; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.2e+07;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ttctgaga 8
   ||| |||
Db 9 TTCCGAAA 2

RESULT 5
HSM007328
ID HSM007328 standard; RNA; EST; 11 BP.
AC AL042478;
XX
SV AL042478.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
RL 12-MAR-1999 (Rel. 59, Last updated, Version 1)
DE Homo sapiens mRNA; EST DKFZp434F1721_r1 (from clone DKFZp434F1721)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
XX
XX [1]
RN Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RP 1-11
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA

```

```

CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH
FT source 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
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SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 48.9%; Score 4.4; DB 60; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcctga 6
   ||| ||
Db 3 TTCGGA 8

RESULT 6
HSM007344 standard; RNA; EST; 11 BP.
XX
AC AL042494;
XX
SV AL042494.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434G1721_r1 (from clone DKFZp434G1721)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
FH Key Location/Qualifiers
FH
FT source 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 48.9%; Score 4.4; DB 60; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcctga 6
   ||| ||
Db 3 TTCGGA 8

RESULT 7
HSM007376 standard; RNA; EST; 11 BP.
XX
AC AL042526;
XX
SV AL042526.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434H0321_r1 (from clone DKFZp434H0321)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
FH Key Location/Qualifiers
FH
FT source 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 48.9%; Score 4.4; DB 60; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcctga 6
   ||| ||
Db 3 TTCGGA 8

RESULT 8
AM250935 11 bp mRNA EST 07-JAN-2000
LOCUS AM250935
DEFINITION 2821359.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821359 3',
mRNA sequence.

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SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 48.9%; Score 4.4; DB 60; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcctga 6
   ||| ||
Db 3 TTCGGA 8

RESULT 7
HSM007376 standard; RNA; EST; 11 BP.
XX
AC AL042526;
XX
SV AL042526.1
XX
DT 12-MAR-1999 (Rel. 59, Created)
DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX
DE Homo sapiens mRNA; EST DKFZp434H0321_r1 (from clone DKFZp434H0321)
XX
KM EST; expressed sequence tag.
XX
OS Homo sapiens (human)
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
FH Key Location/Qualifiers
FH
FT source 1. .11
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_1lb="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
FT
SQ Sequence 11 BP; 2 A; 1 C; 3 G; 5 T; 0 other;

Query Match 48.9%; Score 4.4; DB 60; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ttcctga 6
   ||| ||
Db 3 TTCGGA 8

RESULT 8
AM250935 11 bp mRNA EST 07-JAN-2000
LOCUS AM250935
DEFINITION 2821359.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821359 3',
mRNA sequence.

```

```

ACCESSION   AM250935
VERSION     AM250935.1
KEYWORDS    GI:6593928
SOURCE      EST.
ORGANISM    human.
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 11)
AUTHORS     NIH-MGC http://mgc.ncl.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Other_Estns: 2821359.5prime
            Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: DCTD/DPF cDNA Library Preparation: Ling
            Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
            Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
            project Clone distribution: MGC clone distribution information can
            be found through the I.M.A.G.E. Consortium/LNL at:
            www.bio.lnl.gov/db/rp/image/image.html Base Calling / Quality
            Scores: PHRED from University of Washington Genome Center. Vector
            Trimming: cross match from University of Washington Genome Center
            PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
            Drosophila Genome Project. University of Washington Genome Center:
            http://www.genome.washington.edu Low Quality Sequence: 11
            contiguous PHRED high quality bases following vector sequence. Very
            low Quality Sequence: Trace file contained 11 contiguous distinct
            peaks following vector sequence.
            Plate: L1066 row: J column: 16
            High quality sequence stop: 11.
            Location/Qualifiers
                1..11
                /organism="Homo sapiens"
                /db_xref="taxon:9606"
                /clone_1b="NIH_MGC_7"
                /tissue_type="small cell carcinoma"
                /cell_line="MGC3"
                /lab_host="DH10B (phage-resistant)"
                /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
                EcoRI; cDNA made by oligo-dT priming. Directionally
                cloned into EcoRI/XhoI sites using the following 5'
                adaptor: GGCACGAG(G). Size-selected >500bp for average
                insert size 1.8kb. Library constructed by Ling Hong in
                the laboratory of Gerald M. Rubin (University of
                California, Berkeley) using ZAP-cDNA synthesis kit
                (Stratagene) and Superscript II RT (Life Technologies)."
```

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BASE COUNT      5 a          1 c          4 g          1 t
ORIGIN
Query Match      48.9%; Score 4.4; DB 113; Length 11;
Best Local Similarity 83.3%; Pred. No. 8e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 3 ctgaga 8
    1 ||||
    4 CAGAGA 9
Db
RESULT 9
HSM007404 standard; RNA; EST; 12 BP.
XX AC AL042554.1
XX SV AL042554.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434I0921_r1 (from clone DKFZp434I0921)
```

```

XX XX EST; expressed sequence tag.
KM Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX [1]
RP Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RA Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RT MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
RL
CC Clone from S. Wiemann, sequenced by LMU within the cDNA
CC sequencing consortium of the German Genome Project
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
FH Key Location/Qualifiers
FH 1..12
FT source
FT /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone_1b="DKFZp434I0921"
FT /clone_1b="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NotI + SalI"
FT /dev_stage="adult"
FT /tissue_type="testis"
SQ
Sequence 12 BP; 2 A; 3 C; 3 G; 4 T; 0 other;
Query Match      48.9%; Score 4.4; DB 60; Length 12;
Best Local Similarity 83.3%; Pred. No. 8.1e+07;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 ttctga 6
    1 ||| |
    2 TTTCGA 7
Db
RESULT 10
HSM007404/c
ID HSM007404 standard; RNA; EST; 12 BP.
XX AC AL042554.1
XX SV AL042554.1
XX DT 12-MAR-1999 (Rel. 59, Created)
XX DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX DE Homo sapiens mRNA; EST DKFZp434I0921_r1 (from clone DKFZp434I0921)
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
XX OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
XX OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX [1]
XX 1-12
XX Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
XX Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
XX MIPS, Am Klopferspitz 18a D-82152 Martinsried, GERMANY
XX Clone from S. Wiemann, sequenced by LMU within the cDNA
XX sequencing consortium of the German Genome Project
XX No sl sequence available
```



CC This clone is available at the RZPD in Berlin  
 CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
 CC Berlin-Charlottenburg, GERMANY; Email: cloneerzpd.de

XX Key Location/Qualifiers

FT source 1. .12

FT /db\_xref="taxon:9606"

FT /organism="Homo sapiens"

FT /clone="DKFZp43410921"

FT /clone\_lib="434 (synonym: htes3). Vector pSport1, host

FT DH10B; sites NotI + SalI"

FT /dev\_stage="adult"

FT /tissue\_type="testis"

XX Sequence 12 BP: 2 A; 3 C; 3 G; 4 T; 0 other;

Qy 1 tttctga 6

Db 8 TTCCGA 3

RESULT 11

LOCUS AQ090961 5 bp DNA GSS 09-JAN-2001

DEFINITION GSSrc07954 Trypanosoma cruzi random genomic library Trypanosoma

ACCESSION AQ090961 GI:9371014

VERSION AQ090961.2 GI:9371014

KEYWORDS GSS.

SOURCE Trypanosoma cruzi.

ORGANISM Trypanosoma cruzi.

REFERENCE 1 (bases 1 to 5)

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma

cruzi genome: general structure, large gene and repetitive DNA

families, and gene discovery

Genome Res. 10 (12), 1996-2005 (2000)

20568489

On Jul 21, 2000 this sequence version replaced gi:6490291.

Contact: Sanchez D.O.

Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral

San Martin)

Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24

CP(1650) San Martin, Prov. de BS AS, Argentina

Tel: 54-11-4580-7255 ext 309

Fax: 54-11-4752-9639

Email: dsanchez@ib.unsam.edu.ar

Seq primer: T7

Class: Shotgun.

FEATURES

source

Query Match 44.4%; Score 4; DB 213; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 agaa 9

Db 1 AGAA 4

RESULT 12

LOCUS AQ090961 5 bp DNA GSS 09-JAN-2001

DEFINITION GSSrc07954 Trypanosoma cruzi random genomic library Trypanosoma

ACCESSION AQ090961 GI:9371014

VERSION AQ090961.2 GI:9371014

KEYWORDS GSS.

SOURCE Trypanosoma cruzi.

ORGANISM Trypanosoma cruzi.

REFERENCE 1 (bases 1 to 5)

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma

cruzi genome: general structure, large gene and repetitive DNA

families, and gene discovery

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On Jul 21, 2000 this sequence version replaced gi:6490291.

Contact: Sanchez D.O.

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Tel: 54-11-4580-7255 ext 309

Fax: 54-11-4752-9639

Email: dsanchez@ib.unsam.edu.ar

Seq primer: T7

Class: Shotgun.

FEATURES

source

1. .5

/organism="Trypanosoma cruzi"

/strain="CL-Brener"

/db\_xref="taxon:5693"

/clone="G35F18"

/clone\_lib="Trypanosoma cruzi random genomic library"

/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was

randomly sheared using a nebulizer and the 1 to 2 Kb range

was gel purified and cloned into the dephosphorylated

HincII site of the vector"

Query Match 44.4%; Score 4; DB 213; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+09;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tttct 4

Db 4 TTCT 1

RESULT 13

LOCUS HSM008038 standard; RNA; EST; 9 BP.

DEFINITION HSM008038 standard; RNA; EST; 9 BP.

ACCESSION AL043188;

VERSION AL043188.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.

A random sequencing approach for the analysis of the trypanosoma

cruzi genome: general structure, large gene and repetitive DNA

families, and gene discovery

Genome Res. 10 (12), 1996-2005 (2000)

20568489

On Jul 21, 2000 this sequence version replaced gi:6490291.

Contact: Sanchez D.O.

Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral

San Martin)

Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24

CP(1650) San Martin, Prov. de BS AS, Argentina

Tel: 54-11-4580-7255 ext 309

Fax: 54-11-4752-9639

Email: dsanchez@ib.unsam.edu.ar

Seq primer: T7

Class: Shotgun.

FEATURES

source

1. .5

/organism="Trypanosoma cruzi"

/strain="CL-Brener"

/db\_xref="taxon:5693"

/clone="G35F18"

/clone\_lib="Trypanosoma cruzi random genomic library"

/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was

randomly sheared using a nebulizer and the 1 to 2 Kb range

was gel purified and cloned into the dephosphorylated

HincII site of the vector"

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DT 12-MAR-1999 (Rel. 59, Last updated, Version 1)
XX Homo sapiens mRNA; EST DKFZp434G2223_r1 (from clone DKFZp434G2223)
DE
XX EST; expressed sequence tag.
XX
XX Homo sapiens (human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
XX
XX
RN [1]
RP 1-9
RA Blum H., Bauersachs S., Mewes W., Gassenhuber J., Wiemann S.;
RT Submitted (12-MAR-1999) to the EMBL/GenBank/DBJ databases.
RL MIPS, Am Klopferplatz 18a D-82152 Martinsried, GERMANY
XX
XX
CC Clone from S. Wiemann, sequenced by LMU within the CDNA
CC sequencing consortium of the German Genome Project
CC No s1 sequence available
CC This clone is available at the RZPD in Berlin
CC Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
CC Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
XX
XX
FH Key Location/Qualifiers
FH 1. .9
FT source /db_xref="taxon:9606"
FT /organism="Homo sapiens"
FT /clone="DKFZp434G2223"
FT /clone_lib="434 (synonym: htes3). Vector pSport1; host
FT DH10B; sites NciI + Sali"
FT /dev_stage="adult"
FT /tissue_type="testis"
XX
XX
SQ Sequence 9 BP; 1 A; 1 C; 2 G; 5 T; 0 other:

Query Match 44.4%; Score 4; DB 60; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.7e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctg 5
   |||
   1 TCTG 4

DB

RESULT 14
AM247612/c 11 bp mRNA EST 07-JAN-2000
LOCUS 2819980.5prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2819980 5',
DEFINITION mRNA sequence.
ACCESSION AM247612
VERSION AM247612.1 GI:6590605
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 11)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2819980.3prime
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.nih.gov/db/brp/image/image.html Base Calling / Quality

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```

FEATURES
Source
1. .11
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2819980"
/clone_lib="NIH_MGC_7"
/tissue_type="small cell carcinoma"
/cell_line="MGC3"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(C). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

```

BASE COUNT
ORIGIN
3 a 3 c 4 g 1 t

Query Match 44.4%; Score 4; DB 112; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+08;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 tctg 5
   |||
   1 TCTG 6

DB

RESULT 15
AM250935/c 11 bp mRNA EST 07-JAN-2000
LOCUS 2821359.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2821359 3',
DEFINITION mRNA sequence.
ACCESSION AM250935
VERSION AM250935.1 GI:6593928
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 11)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Other ESTs: 2821359.5prime
Contact: Robert Strausberg, Ph.D.
Tel.: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: DCTD/DRP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LNL) DNA Sequencing by: Berkeley MGC sequencing
project clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.lnl.nih.gov/db/brp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
trimming: cross_match from University of Washington Genome Center
PHRAP suite. Poly-T identification: patmatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 0 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: trace file contained 11 contiguous distinct peaks
following vector sequence.
Plate: LCM3 row: A column: 5.

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Plate: L1CM6 row: J column: 16  
High quality sequence stop: 11.

FEATURES  
Location/Qualifiers  
1. 11

source  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2821359"  
/clone\_lib="NIH\_MGC\_7"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: lung; Vector: pORF7; Site\_1: XhoI; Site\_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(C). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT  
5 a 1 c 4 g 1 t  
ORIGIN

Query Match 44.4%; Score 4; DB 113; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.5e+08;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 tctg 5  
1111  
Db 7 TCTG 4

Search completed: April 21, 2001, 12:34:38  
Job time: 4794 sec

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